Amendments to the Specification:

Following the Abstract, please replace the Sequence Listing with the attached replacement Sequence Listing, with subsequent page numbering thereafter.

Please delete paragraph [00011] on page 4 and replace with the following amended paragraph:

[00011] The co-crystal determined that the EVH1 fold is isomorphic to the plextrin homology (PH) domain (Figure 1). The co-crystal also identified surfaces of interaction with the Homer ligand and rationalized the consensus sequence of the Homer ligand. Critical sites of contact include an association between the second proline (TPPSPF, SEQ ID NO: 2) and tryptophan W24 in the Homer 1 EVH1, and between the phenylalanine and a pocket that extends to glycine 89 of the EVH1 domain (Beneken et al., 2000). The critical contribution of these sites of interaction to the overall energetics of binding was confirmed in assays of binding that used point mutants of the EVH1 domain. The crystal also indicated that the original consensus sequence PPXXFR ([~~SEQ ID NO:3~~] SEQ ID NO:21) should be modified to PXXF ([~~SEQ ID NO:4~~] SEQ ID NO:3) since the first proline is not essential for contact with the EVH1 domain. The first proline may contribute to the overall conformation of the local protein sequence. The contact at the second proline involves the amino acid backbone and not the proline side chain, so other amino acids could, in principle, substitute for proline. Additional prolines are common in natural Homer ligands and are rationalized to be important in defining the correct configuration of the ligand for binding, but not in direct contact with the EVH1 binding surface. Perhaps most importantly, the co-crystal demonstrated that the binding surface of the proline is similar to that of related EVH1 domains of Ena, Mena and Vasp, but the surface for the phenylalanine is unique to the Homer subfamily. Thus, it has been concluded that the Homer genes are a subfamily of the EVH1 family which possess unique binding surfaces and ligand sequence recognition.

Please delete paragraph [00081] on page 19 and replace with the following amended paragraph:

[00081] An example of a protein containing such proline-type Homer consensus sequence includes, but is not limited to, synphilin (e.g., Acc. No. NP005451, SEQ ID NO:31), EF2kinase (e.g., NP037434, SEQ ID NO:32), p70 (e.g., Acc. No. AAB97097, SEQ ID NO:33), Notch 4 (e.g., NP004548, SEQ ID NO:34), AGE-BP1 (e.g., Q00900, SEQ ID NO:35), cytosolic thymidine kinase (e.g., Acc. No. NP003249, SEQ ID NO:36), neuronal PAS domain protein 2 (e.g., NP840084, SEQ ID NO:37), zona pellucida sperm binding protein 3 precursor (e.g., NP009086, SEQ ID NO:38), Shank family of proteins (e.g., Acc. Nos. Q9JLU4, SEQ ID NO:39; NP113939, SEQ ID NO:40; NP067708, SEQ ID NO:41; Q9WV48, SEQ ID NO:42; P97836, SEQ ID NO:43; AAF61375 SEQ ID NO:44; and AAD29417 SEQ ID NO:45), ryanodine receptor (e.g., [[Ace.]] Acc. No. NP000531, SEQ ID NO:46), p82 (e.g., Acc. No. AAC50926, SEQ ID NO:47), androgen receptor (e.g., Acc. No. P10275, SEQ ID NO:48), TrpC1 (e.g., Acc. Nos. NP776901, SEQ ID NO:49; NP003295, SEQ ID NO:50; NP057263 SEQ ID NO:51), mGluR1a (e.g., Acc. No. NP000829, SEQ ID NO:52) or mGluR5 (e.g., Acc. No. BAA05891, SEQ ID NO:53).

Please delete paragraph [00098] on page 23 and replace with the following amended paragraph:

[00098] Moreover, Homer protein sequences may include, but are not limited to, sequences as set forth in the following accession numbers: NP004829, SEQ ID NO:54; NP004830, SEQ ID NO:55; NP004263, SEQ ID NO:56; NP671705, SEQ ID NO:57; NP445762 SEQ ID NO:58; and NP445761 SEQ ID NO:59.

Please delete paragraph [00099] on page 23 and replace with the following amended paragraph:

[00099] Thus, looking at the N-terminal region of the polypeptides [~~shown in FIG. –~~], it is apparent that the first 30 amino acids are invariant among the three sequences. However, positions 31-34 differ. The rat sequence is AVTV (SEQ ID NO:11), while the human and mouse proteins share the sequence GHRF (SEQ ID NO:12). From this variation, it is possible to

construct polypeptides in which positions 31-34 have the variable sequences: A/G V/H T/R V/F. Further regions of variability are apparent from inspection of the aligned sequences. Certain regions of the rat Homer protein have been identified as significant in the context of its function. For example, the PDZ-like domain GLGF sequence and preceding arginine at positions 87-90 and 81, respectively, may form a "binding pocket", based on the known binding pocket of the synaptic binding protein PSD95 (Kornau, et al., 1995). In accordance with the foregoing guidelines concerning substitution, this region is invariant among the three exemplified synaptic activation proteins and should therefore be conserved in any sequences deduced from these proteins.

Please delete paragraph [000103] on page 24 and replace with the following amended paragraph:

[000103] For example, the bacterially expressed GST-Homer fusion protein was tested for binding to native mGluR5 in detergent extracts of hippocampus in an in vitro binding assay. [~~As shown in FIG. _~~,] mGluR5 binds to GST-Homer fusion protein, but not to GST alone. GST-Homer pull down assays can use purified proteins, recombinant proteins in heterologous cells, native proteins from cell lines or primary cultures or whole animals. For these assays, point mutants of homer (W24A or G89N mutants of Homer 1 or equivalent mutants in Homer 2 or 3) provide informative negative controls (Beneken et al., 2000). Effects on Homer interaction with target proteins can also be assayed by co-immunoprecipitation (co-IP) from the same protein sources (see below).